

AGAAGTGATG	CCACTTGGTT	AAGGTCCCAG	AGCAGGTCAG	AATCAGACCT	AGGATCAGAA	60						
ACCTGGCTCC	TGGCTCCTGG	CTCCCTACTC	TTCTAAGGAT	CGCTGTCCTG	ACAGAAGAGA	120						
ACTCCTCTTT	CCTAAA	ATG GAG	TCG AGT	AAA AAG	ATG GAC	TCT CCT	GGC	169				
		Met	Glu	Ser	Ser	Lys	Lys	Met	Asp	Ser	Pro	Gly
		1				5					10	
GCG CTG	CAG ACT	AAC CCG	CCG CTA	AAG CTG	CAC ACT	GAC CGC	AGT GCT	217				
Ala Leu	Gln Thr	Asn Pro	Pro Leu	Lys Leu	His Thr	Asp Arg	Ser Ala					
	15			20		25						

GGG Gly	ACG Thr	CCA Pro 30	GTT Val	T P	TC al	CCT Pro	GAA Glu 35	CAA Gln	GGA Gly	GGT Gly	TAC Tyr	AAA Lys 40	AAA Lys	AAG Lys	TTT Phe	265
GTG Val	AAG Lys 45	ACC Thr	GTG Val	GAG Glu	GAC Asp	AAG Lys 50	TAC Tyr	AAG Lys	TGT Cys	GAG Glu	AAG Lys 55	TGC Cys	CAC His	CTG Leu	GTG Val	313
CTG Leu 60	TGC Cys	AGC Ser	CCG Pro	AAG Lys	CAG Gln 65	ACC Thr	GAG Glu	TGT Cys	GGG Gly	CAC His 70	CGC Arg	TCC Ser	TGC Cys	GAG Glu	AGC Ser 75	361
TGC Cys	ATG Met	GCG Ala	GCC Ala	CTG Leu 80	CTG Leu	AGC Ser	TCT Ser	TCA Ser	AGT Ser 85	CCA Pro	AAA Lys	TGT Cys	ACA Thr	GCG Ala 90	TGT Cys	409
CAA Gln	GAG Glu	AGC Ser	ATC Ile 95	GTT Val	AAA Lys	GAT Asp	AAG Lys	GTG Val 100	TTT Phe	AAG Lys	GAT Asp	AAT Asn 105	TGC Cys 105	TGC Cys	AAG Lys	457
AGA Arg	GAA Glu 110	ATT Ile	CTG Leu	GCT Ala	CTT Leu	CAG Gln	ATC Ile 115	TAT Tyr	TGT Cys	CGG Arg	AAT Asn	GAA Glu 120	AGC Ser	AGA Arg	GGT Gly	505
TGT Cys	GCA Ala 125	GAG Glu	CAG Gln	TTA Leu	ACG Thr	CTG Leu 130	GGA Gly	CAT His	CTG Leu	CTG Leu	GTG Val 135	CAT His	TTA Leu	AAA Lys	AAT Asn	553
GAT Asp 140	TGC Cys	CAT His	TTT Phe	GAA Glu 145	GAA Glu	CTT Leu	CCA Pro	TGT Cys	GTG Val	CGT Arg 150	CCT Pro	GAC Asp	TGC Cys	AAA Lys	GAA Glu 155	601
AAG Lys	GTC Val	TTG Leu	AGG Arg	AAA Lys 160	GAC Asp	CTG Leu	CGA Arg	GAC Asp	CAC His 165	GTG Val	GAG Glu	AAG Lys	GCG Ala	TGT Cys 170	AAA Lys	649
TAC Tyr	CGG Arg	GAA Glu	GCC Ala 175	ACA Thr	TGC Cys	AGC Ser	CAC His	TGC Cys 180	AAG Lys	AGT Ser	CAG Gln	GTT Val 185	CCG Pro	ATG Met	ATC Ile	697
GCG Ala	CTG Leu	CAG Gln 190	AAA Lys	CAC His	GAA Glu	GAC Asp	ACC Thr 195	GAC Asp	TGT Cys	CCC Pro	TGC Cys	GTG Val 200	GTG Val	GTG Val	TCC Ser	745
TGC Cys	CCT Pro 205	CAC His	AAG Lys	TGC Cys	AGC Ser	GTC Val 210	CAG Gln	ACT Thr	CTC Leu	CTG Leu	AGG Arg 215	AGC Ser	GAG Glu	GGG Gly	ACA Thr	793
AAC Asn 220	CAG Gln	CAG Gln	ATC Ile	AAG Lys	GCC Ala 225	CAC His	GAG Glu	GCC Ala	AGC Ser	TCC Ser 230	GCC Ala	GTG Val	CAG Gln	CAC His	GTC Val 235	841
AAC Asn	CTG Leu	CTG Leu	AAG Lys	GAG Glu 240	TGG Trp	AGC Ser	AAC Asn	TCG Ser	CTC Leu 245	GAA Glu	AAG Lys	AAG Lys	GTT Val 250	TCC Ser	TTG Leu	889
TTG Leu	CAG Gln	AAT Asn	GAA Glu 255	AGT Ser	GTA Val	GAA Glu	AAA Lys	AAC Asn 260	AAG Lys	AGC Ser	ATA Ile	CAA Gln 265	AGT Ser 265	TTG Leu	CAC His	937
AAT Asn	CAG Gln	ATA Ile 270	TGT Cys	AGC Ser	TTT Phe	GAA Glu	ATT Ile 275	GAA Glu	ATT Ile	GAG Glu	AGA Arg	CAA Gln 280	AAG Lys	GAA Glu	ATG Met	985
CTT Leu	CGA Arg 285	AAT Asn	AAT Asn	GAA Glu	TCC Ser	AAA Lys 290	ATC Ile	CTT Leu	CAT His	TTA Leu 295	CAG Gln	CGA Arg	GTG Val	ATA Ile	GAC Asp	1033

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CACCTGACAC GTTTTAT T AGACTAGCCA CACTTCACTC TGAAGA A TTTATCCTTC 1986  
AACAAGCATA AATATTG G TCAGAGAAGG TTTTCATTTT CATTTTAA GATCTAGTTA 2046  
ATTAAGGTGG AAAACATATA TGCTAAACAA AAGAAACATG ATTTTCTTC CTAAACTTG 2106  
AACACCAAAA AACACACACA CACACACACA CGTGGGGATA GCTGGACATG TCAGCATGTT 2166  
AAGTAAAAGG AGAATTTATG AAATAGTAAT GCAATTCTGA TATCTTCTTT CTAAATTC A 2226  
AGAGTGCAAT TTTG 2240

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn  
1 5 10 15  
Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe  
20 25 30  
Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu  
35 40 45  
Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys  
50 55 60  
Gln Thr Glu Cys Gly His Arg Ser Cys Glu Ser Cys Met Ala Ala Leu  
65 70 75 80  
Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val  
85 90 95  
Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala  
100 105 110  
Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu  
115 120 125  
Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu  
130 135 140  
Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys  
145 150 155 160  
Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr  
165 170 175  
Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His  
180 185 190  
Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys  
195 200 205  
Ser Val Gln Thr Leu Leu Arg Ser Glu Gly Thr Asn Gln Gln Ile Lys  
210 215 220

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Ala His Glu Ala S er Ala Val Gln His Val Asn Leu Lys Glu  
 225 30 235 240  
 Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu Leu Gln Asn Glu Ser  
 245 250 255  
 Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His Asn Gln Ile Cys Ser  
 260 265 270  
 Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met Leu Arg Asn Asn Glu  
 275 280 285  
 Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp Ser Gln Ala Glu Lys  
 290 295 300  
 Leu Lys Glu Leu Asp Lys Glu Ile Arg Ser Phe Arg Gln Asn Trp Glu  
 305 310 315 320  
 Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln Asn Arg Val  
 325 330 335  
 Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Val Ala Arg Asn  
 340 345 350  
 Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln Met Leu Ser  
 355 360 365  
 Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Arg Phe Gln Val Leu  
 370 375 380  
 Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr  
 385 390 395 400  
 Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu Ser Leu Tyr  
 405 410 415  
 Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg  
 420 425 430  
 Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His Leu Ser Leu  
 435 440 445  
 Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro  
 450 455 460  
 Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly Ser Ser Arg  
 465 470 475 480  
 Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe  
 485 490 495  
 Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe  
 500 505 510  
 Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr  
 515 520 525  
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## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCAAA AAGGTGGCCA AG

22

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGATCATCAC TGTCTCTCCT GCAC

24

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAATTCAAG GCCCCCACC CCAAG

25

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGATCAACTC TCTTTGCCAT CCTC

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## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAATTCAAG AGAAAGGAAG TACAG

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## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGATCACTA GACCAAGCTT TGGAT

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## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAATTCAAA AAGAAGCCCT TGTGCCT

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## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTCGACTTA ACTGGGCTTC ATCCCA

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